

**Figure 1**  
**Interleukin-21**

**Figure 2A**  
**Interleukin-22**

1 GGAATTCCGCACGGAGCTCGTGCCTGCTCAGTGCCTTCACACACGCTGCAGCTGGGC	60	
1 N S A R A R A V L S A F H H T L Q L G P	20	
#		
61 CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCGCAGGGGCAGGGCCGACCGCCGCT	120	
21 R E Q A R N A S C P A G G R P A D R R F	40	
121 TCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCTGGCCTACAGAATCTCCTACGACC		180
41 R P P T N L R S V S P W A Y R I S X D P	60	
<i>Domain I</i>		
181 CGGCGAGGTACCCCAGGTACCTGCCTGAAGCCTACTGCCCTGTGCCGGCTGCCTGACCG	240	
61 <u>A R Y P R Y L P E A Y C L C R G C L T G</u>	80	
<i>Domain I</i> <i>Domain II</i>		
241 GGCTGTTGGCGAGGAGGACGTGCCTTCCGCAGCGCCCCCTGTCTACATGCCACCGTCG	300	
81 L F G E E D V R F R S A P V Y M P T V V	100	
<i>Domain III</i>		
301 TCCTGCCCGCACCCCCCGCTGCCCGGCCGTTCCGCTACACCGAGGCCTACGTCA	360	
101 <u>L R R T P A C A G G R S V Y T E A Y V T</u>	120	
<i>Domain III</i>		
#		
361 CCATCCCCGTGGGCTGCACCTGGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCACT	420	
121 <u>I P V G C T C V P E P E K D A D S I N S</u>	140	
<i>Domain IV</i>		
421 CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGCCCCAACGACGGCGCCGCTGGCC	480	
141 S I D K Q G A K L L L G P N D A P A G P	160	
481 CCTGAGGCCGGTCTGCCCGGGAGGTCTCCCGGGCCGATCCGAGGCCAACGCTG		540
541 GAGCCGCCTGGAGGGCTGGTGGACCTCTGAAGAGAGTCACCGAGCAAACCAAGTG	600	
601 CCGGAGCACCGCGCCCTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGCA	660	
661 TCCCTGGCTTGCCTTCTAGCTACAAGCAAGCAGCGTGGCTGGAAAGCTGATGGAAACGACC	720	
721 CGGCACGGGATCCTGTGTGGGCCGATGGAGGGTTGGAAAAGTCACGGAGGCTCC	780	
781 CTGAGGAGCCTCTCAGATCGGCTGCTGCCGGTGCAGGGCGTGACTCACCGCTGGGTGCTT	840	
841 GCCAAAGAGATAGGGACGCATATGCTTTAAAGCAATCTAAAAATAATAAGTATAG	900	

Figure 2B  
Interleukin-22

901 CGACTATATACCTACTTTTAAATCAACTGTTTGAATAGAGGCAGAGCTATTTTATATT 960  
961 ATCAAATGAGAGCTACTCTGTTACATTTCTAACATATAAACATCGTTTTTACTCTTC 1020  
1021 TGGTAGAATTTTTAAAGCATAATTGGAATCCTGGATAAATTTGTAGCTGGTACACTC 1080  
1081 TGGCCTGGGTCTCTGAATTCAAGCCTGTACCGATGGCTGACTGATGAAATGGACACGTCT 1140  
1141 CATCTGACCCACTCTCCCTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG 1200  
1201 ATGCACAGGCGGCTCGATGCCCAAGGGCCAGCTAAGAGTTCAAAGATCTCAGATTGG 1260  
1261 TTTTAGTCATGAATAACATAAACAGTCTCAAACCTGCACAATTCCCCCTTTGAAAG 1320  
1321 CCACTGGGCCAATTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGAACGTGACATCTT 1380  
1381 GCCAGTTGTCAGAAGAACCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTGTAGGATCAGG 1440  
1441 CTGAATATGAGGACAAAGTGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTCT 1500  
1501 GTTTCTGCATTCTGCCACGAGAGCTAGGTCTTGATCTTTCTTAGATTGAAAGTCTGT 1560  
1561 CTCTGAACACAATTATTGTAAAAGTTAGTAGTTCTTTAAATCATTAAAAGAGGCTT 1620  
1621 GCTGAAAAAAAAAAAAAAA 1642

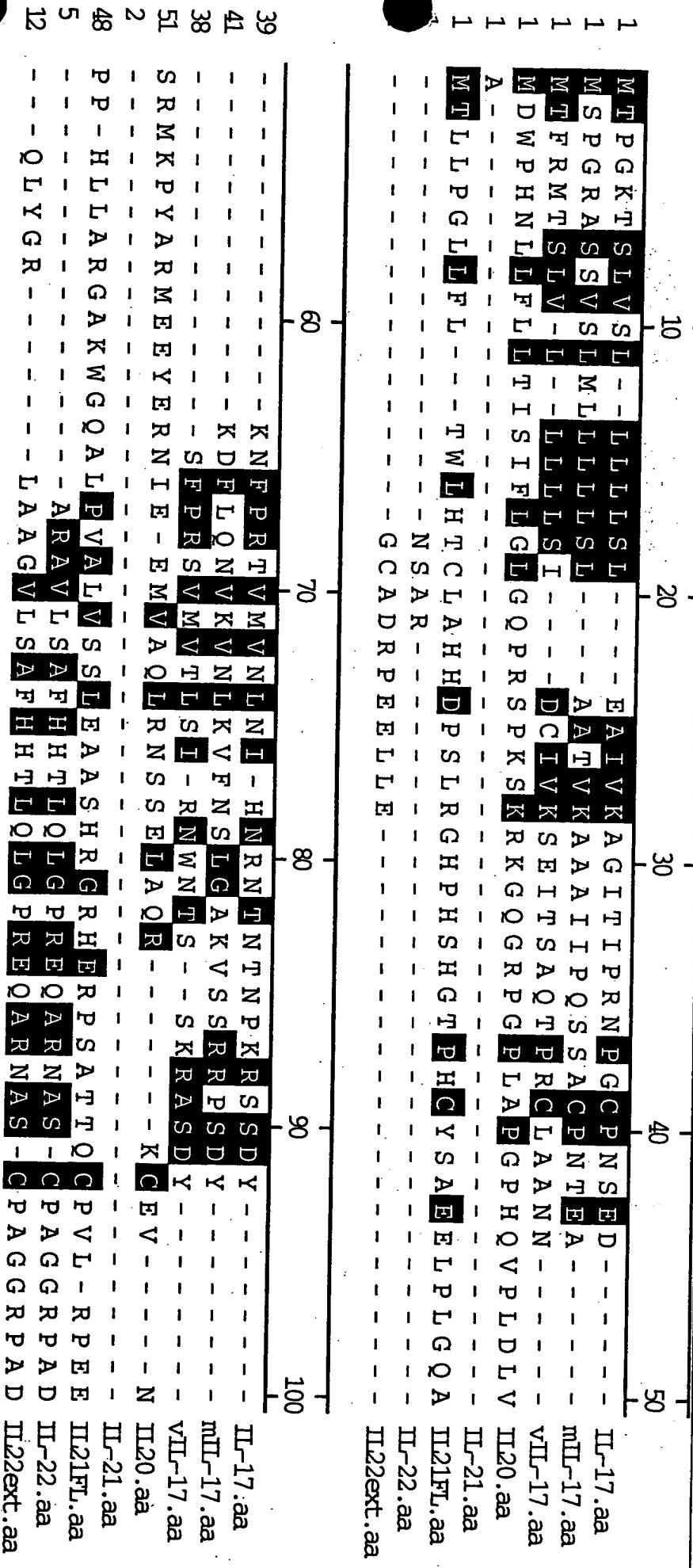


Figure 3A

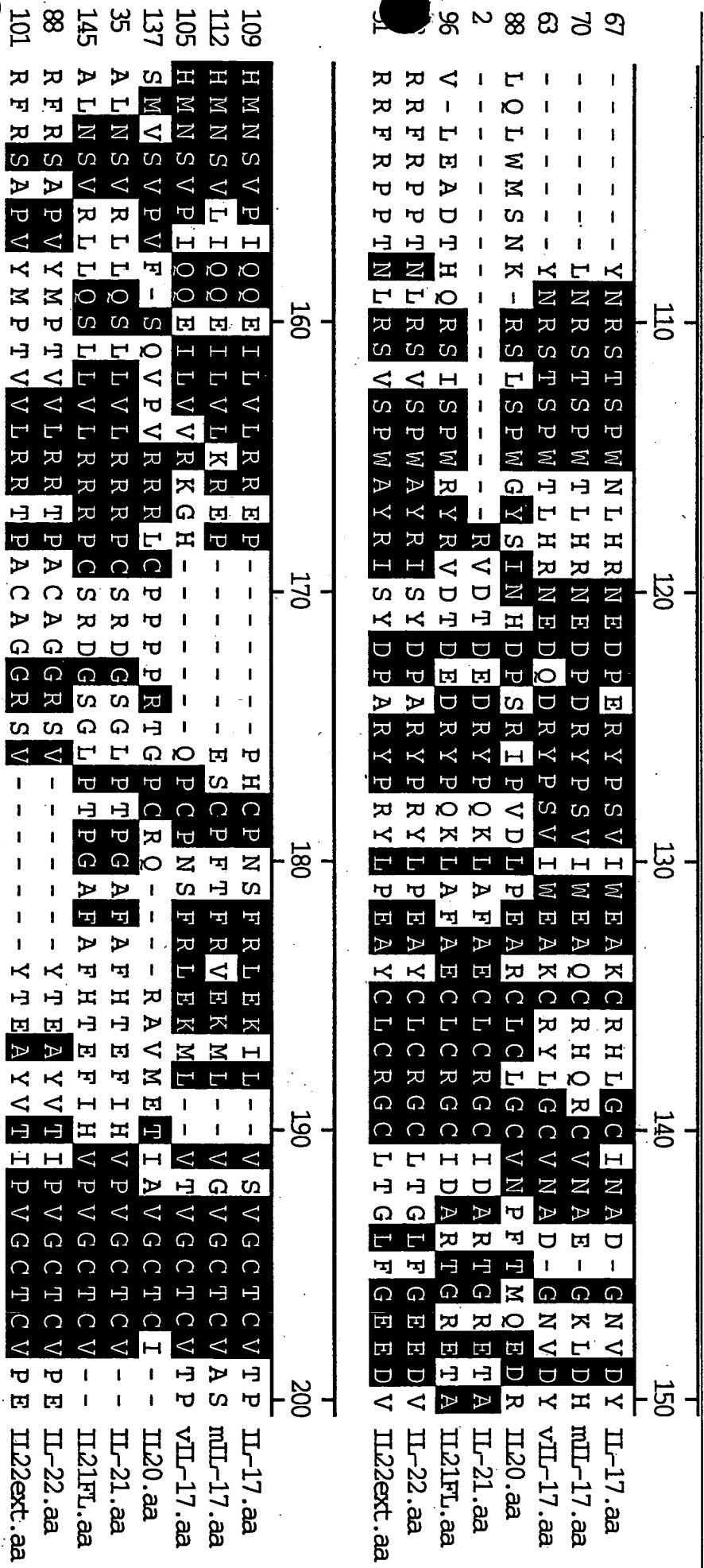


Figure 3B

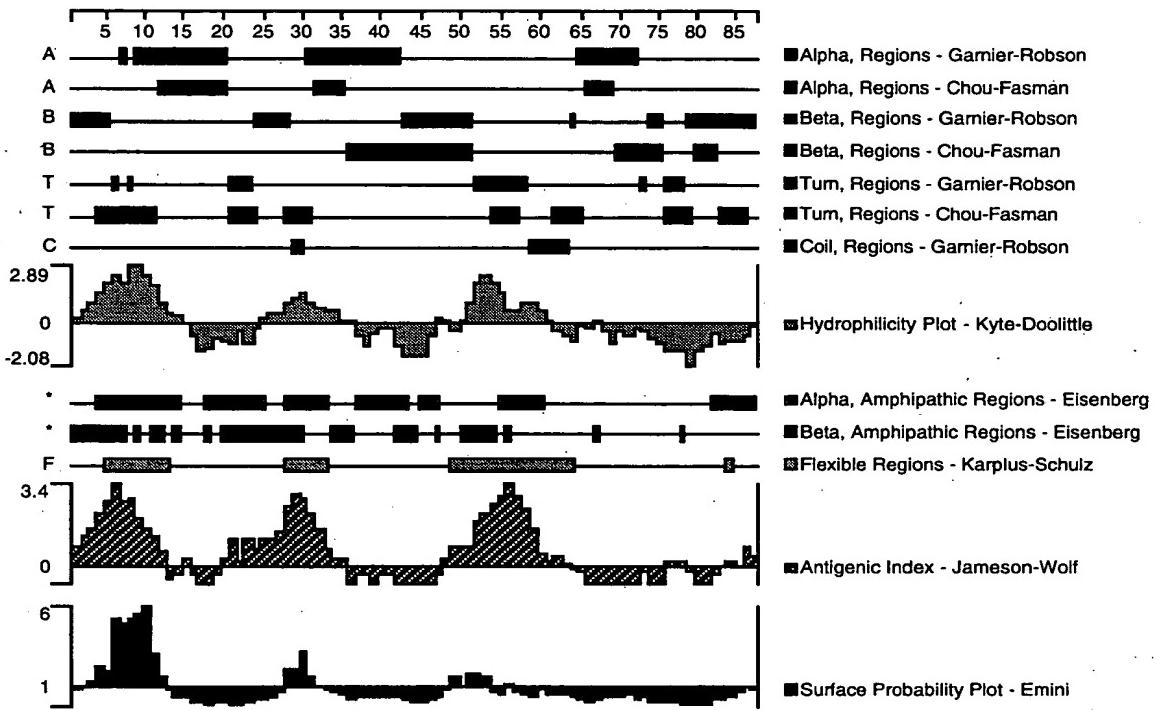
150 I V H H V A  
153 I V R Q A A  
146 I V H N V D  
180 - - - - -  
83 - - - - -  
193 - - - - -  
31 P E K D A D S I N S S I D K Q G A K I L L G P N D A P A G P  
44 P E K D A D S I N S S I D K Q G A K I L L G P N D A P A G P

210 | 220 | 230 |

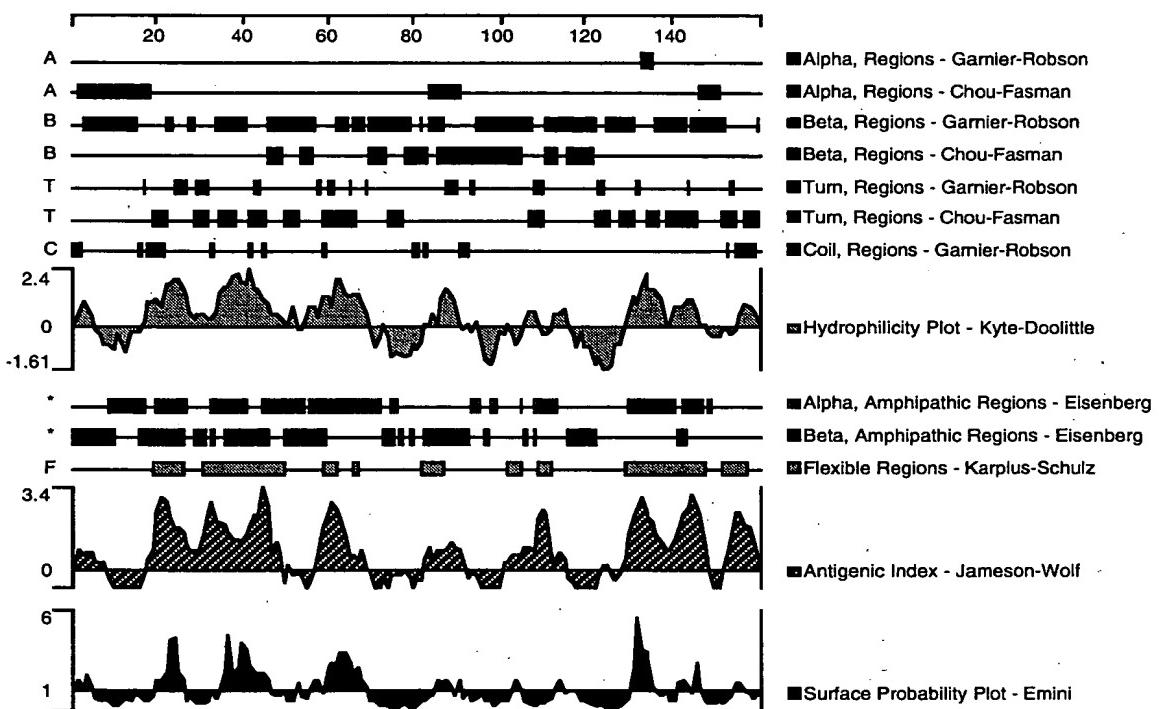
IL-17.aa  
mIL-17.aa  
vIL-17.aa  
IL20.aa  
IL-21.aa  
IL21FL.aa  
IL-22.aa  
IL22ext.aa

Figure 3C

**Figure 4**  
**Interleukin-21 Polypeptide Analysis**



**Figure 5**  
**Interleukin-22 Polypeptide Analysis**

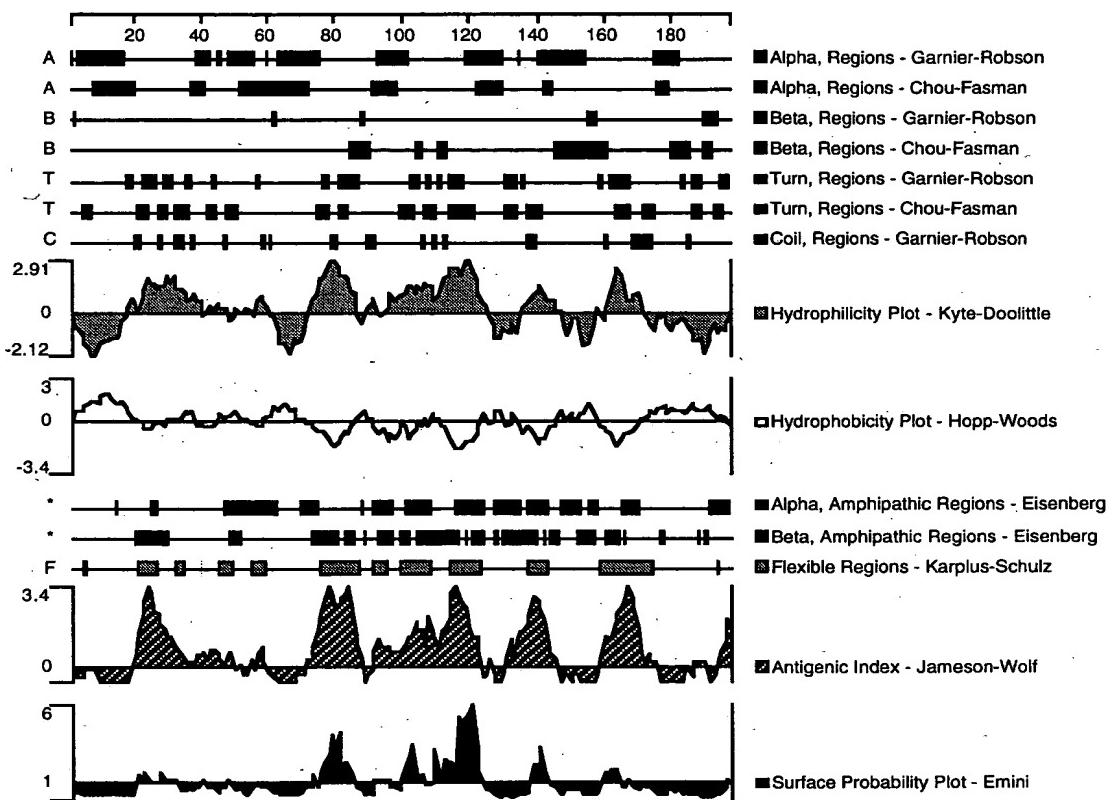


**Figure 6A**  
**Interleukin-21**

1	GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCGGCCCTCCGTGTTT	M T L L P G L L F	60 9
61	CTGACCTGGCTGCACACATGCCCTGGCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC	L T W L H T C L A H H D P S L R G H P H	120 29
10			
121	AGTCACGGTACCCACACTGCTACTCGCTGACGAACGTGCCCTCGGCCAGGGCCCCCA	S H G T P H C Y S A E E L P L G Q A P P	180 49
30			
	Domain V		
181	CACCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGCTTGCCCTGTAGCCCTGGTGTCCAGC	H L L A R G A K W G Q A L P V A L V S S	240 69
50			
	Domain VI		
241	CTGGAGGCAGCAAGCCACAGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG	L E A A S H R G R H E R P S A T T Q C P	300 89
70			
301	GTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGG	V L R P E E V L E A D T H Q R S I S P W	360 109
90			
	Domain VII		
361	AGATACGGGTGGACACGGATGAGGACCGCTATCCACAGAACGCTGGCTTCGCCGAGTC	R Y R V D T D E D R Y P Q K L A F A E C	420 129
110			
	Domain I	Domain II	
421	CTGTGCAGAGGCTGTATCGATGCACGGACGGCCGGAGACAGCTGCCTCAACTCCGTG	L C R G C I D A R T G R E T A A L N S V	480 149
130			
	Domain II		
481	CGGCTGCTCCAGAGCCTGCTGGTGTGGCCGCCCTGCTCCCGCGACGGCTCGGGG	R L L Q S L L V L R R R P C S R D G S G	540 169
150			
	Domain III		
541	CTCCCCACACCTGGGGCCTTGCCCTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGC	L P T P G A F A F H T E F I H V P V G C	600 189
170			
	Domain IV		
601	ACCTGCGTGTGCCCCGTTCAAGTGTGACCGCCAAGGCCGTGGGCCCTTAGACTGGACAC	T C V L P R S V	660 197
190			
	Domain IV		
661	GTGTGCTCCCCAGAGGGCACCCCTATTATGTGTATTATTGTATTATATGCCCTCCC		720
721	CCAAACACTACCCCTGGGGCTGGGCATCCCCGTGTGGAGGACAGCCCCCACTGTC		780

**Figure 6B**  
**Interleukin-21**

**Figure 7**  
**Interleukin-21 Polypeptide Analysis**



**Figure 8**  
**Interleukin-22**

1	GGCTGCGCGGACCGCCGGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGC	60
1	G C A D R P E E L L E Q L Y G R L <u>A A G</u>	20
	CD-VI	
	#	
61	GTGCTCAGTGCCTTCACCACACGCTGCAGCTGGGCGCGTGAGCAGGCGCGAACGCG	120
21	<u>V L S A F H H T L Q L G P R E Q A R N A</u>	40
	CD-VI	
121	AGCTGCCGGCAGGGGGCAGGCCGCCGACCGCCGTTCCGGCCGCCACCAACCTGCGC	180
41	<u>S C P A G G R P A D R R F R P P T N L R</u>	60
181	AGCGTGTGCCCTGGCCTACAGAAATCTCTACGACCCGGCGAGGTACCCAGGTACCTG	240
61	<u>S V S P W A Y R I S Y D P A R Y P R Y L</u>	80
	CD-VII	
	CD-I	
241	CCTGAAGCCTACTGCCGTGCCCCGGCTGCCGTGACCGGGCTTCCGGCGAGGAGCGTG	300
81	P E A Y <u>C L C R G C L T G L F G E E D V</u>	100
	CD-II	
301	CGCTTCGGCAGGCCCTGTCTACATGCCACCGTCGTCTGCCGCCACCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P A C</u>	120
	CD-III	
361	GCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGCTGCACCTGC	420
121	A G G R S V Y T E A Y V T <u>I P V G C T C</u>	140
	CD-IV	
	#	
421	GTCCCCGAGCCGGAGAAGGACGCGAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V P E P E K D A D S I N S S I D K Q G A</u>	160
	CD-IV	
481	AAGCTCTGCTGGGCCCAACGACGCCCTGGCCCTGA	522
161	K L L L G P N D A P A G P	174

**Figure 9**  
**Interleukin-22 Polypeptide Analysis**

